

**In the Specification:**

Please amend the specification as shown:

Please delete the paragraph on page 5, line 15 to page 6, line 4 and replace it with the following paragraph:

Figure 1A shows the DNA sequences of exon 1, intron 1 (**SEQ ID NO: 17**), and exon 2 (**SEQ ID NO: 16**) of human Cox-1, as published in the NCBI human genomic database. Figure 1B shows that none of the three reading frames (a, b, and c) results in a polypeptide that comprises the amino acid sequences encoded by exon 1, intron 1, and exon 2. A termination of translation is indicated by a \*. The nucleotide sequences of exon 1 and exon 2, and their encoded amino acid sequences as in Cox-1 are shaded. **Figure discloses SEQ ID NO: 18 coding SEQ ID NOS: 19-22, respectively, in order of appearance.** Figure 1C shows translation of Cox-3a after RNA editing (**SEQ ID NO: 23 coding SEQ ID NO: 24**). Figure 1D shows translation of Cox-3b after RNA editing (**SEQ ID NO: 25 coding SEQ ID NO: 26**). Figure 1E shows a comparison of peptide sequences encoded by COX-1 intron 1 in human and canine COX-3 with (human) or without (canine) RNA editing (**SEQ ID NOS: 27, 4 and 6, respectively, in order of appearance**). The alignment was performed using the algorithm of Needleman and Wunsch to find the alignment of two complete sequences. The alignment maximizes the number of matches and minimizes the number of gaps. Match display thresholds for the alignment(s): | = IDENTITY; : = 2; . = 1. Figure 2 illustrates gene structure of human COX-3 and COX-1.